REVIEWER INDEX

to Volume 127, January–April, 1991

Below is a list of the people who reviewed manuscripts for GENETICS during the preparation of Volume 127. The aim of GENETICS is to communicate significant research. To succeed, we must recognize what is significant, making sure the presentation is accurate, unambiguous and easily readable. For this, we depend heavily on our reviewers, who perform this indispensable service without reward. The quality of the journal strongly reflects the quality of their efforts. We apologize to any reviewer whose name has been inadvertently omitted, and we are sincerely grateful to all.

Albertini, R. J.
Aquadro, C. F.
Asmussen, M. A.

Bailis, A.
Barton, N.
Beach, D.
Berget, P. B.
Berry, A.
Bingham, P. M.
Birchler, J. A.
Boswell, R.
Bostian, K. A.
Brandriss, M.
Brookfield, J. F. Y.
Brower, D.
Bull, J. J.
Bussey, H.

Carlson, W. R.
Caten, C. E.
Chakraborty. R.
Chandlee, J. M.
Chapman, V.
Charlesworth, B.
Cherbas, L.
Clark, A. J.
Coe, E. H.
Cockerham, C. C.
Coyne, J. A.
Craig, E.
Cronmiller, C.
Crosby, M. A.

Davisson, M.
Dawson, D.
Devlin, B.
Ditta, G.
Donahue, D. F.
Doolittle, R. F.
Dutton, F. L.

Eanes, W. F.
Easteal, S.
Egel, R.
Eickbush, T. H.
Erhart, M. A.
Erickson, R. P.

Fangman, W. L.
Felsenstein, J.
Ferrari, J.
Foster, P. L.
Frank, S.
Frisardi, M.

Galloway, R. E.
Ganetzky, B.
Gibson, J. B.
Gillham, N. W.
Gimmelfarb, A.
Glass, N. L.
Goddard, K.
Golding, G. B.
Goodenough, U.
Gottesman, S.
Green, L.
Griffiths, R. C.

Haber, J. E.
Hall, H. G.
Harris, E. H.
Hawley, R. S.
Herskowitz, I.
Hill, C.
Hilliker, A. J.
Hollingsworth, N.
Houle, D.
Hughes, A.

Irick, H.
Iverson, L.

Jenness, D.
Jinks-Robertson, S.

Käfer, E.
Kaplan, N. L.
Keil, R.
Kirkpatrick, M.
Klar, A. J. S.
Klein, H.
Kleinhofs, A.
Knapp, S. J.
Kobayashi, I.
Kohli, J.
Kolodner, R.
Kreitman, M. E.
Krider, H.

Lawrence, C.
Lee, R. W.
Levine, L.
Lewis, S.
Lim, J. K.
Livingston, D.
Long, J. C.
Lyttle, T. W.

Malone, R. E.
Martindale, D.
Matters, G.
Matthews, K.
May, B.
McCarron, M.
Meisler, M.
Merriam, J. R.
Michaelis, S.
Miller, E. S.
Miller, J.
Moehle, C.
Mortin, M.
Muskavitch, M. A. T.

Nadeau, J.
Nagylaki, T.
Nasmyth, K.
Nelson, O. E.
Newlon, C.
Newton, K.

Oaks, A.
O'Donnell, J. M.
Oliver, B.
Orias, E.
Orr, H. A.

Palter, K.
Pardue, M. L.
Parson, P. A.
Partridge, L.
Perrimon, N.
Poteete, A.
Poyton, R. O.
Prout, T.

Radman, M.
Riley, M.
Rinchik, E. M.
Rine, J.
Ritland, K.
Roberts, J. D.
Robertson, D. S.
Robertson, H.
Ronald, P.

Sanicola, M.
Sawyer, S.
Schaeffer, S.
Scherer, S.
Schimenti, J.
Schmidt, R. J.
Schoen, D.
Schwarz, T.
Segraves, W. A.
Sharp, P. M.
Shin, H.-S.
Signer, E.
Silver, L.
Sites, J. W.
Skinner, S.
Smith, D.
Smith, P. D.
Smouse, P. E.
Somers, D. A.
Somerville, C.
Spradling, A. C.
Stahl, F. W.
Stephan, W.
Stewart, S.
Strausbaugh, L.
Stuber, C. W.
Symington, L.
Szostak, J. W.

Tavaré, S.
Thaler, D. S.
Tolias, P.

Walker, J.
Walsh, J. B.
Watt, W. B.
Weber, K. E.
Weinstock, G.
Whitt, G. S.
Whittam, T. S.
Wu, C.-I.

Yoder, O.

Zakian, V.
Zeng, Z.-B.

AUTHOR INDEX

to Volume 127, January–April 1991

Acevedo, A., 601
Aguilera, A., 75
Agulnik, A., 161, 781
Agulnik, S., 781
Allgood, N. D., 671
Ausubel, F. M., 789
Avise, J. C., 391

Baker, B. S., 125
Barton, N. H., 229
Bell, J. C., 619
Bender, W., 139, 739
Bennoun, P., 335
Berg, C. A., 515
Berg, D. E., 649
Birchler, J. A., 609
Birky, C. W., Jr., 449
Bonaduce, M. J., 489
Boyes, D. C., 221
Bryant, P. J., 525
Burke, D. J., 463

Cafferkey, R., 489
Cambareri, E. B., 699
Campbell, S. D., 367
Caplan, S., 299
Casjens, S., 637
Chakravarti, A., 399
Chandler, V. L., 205
Charles, T. C., 5
Charpentier, A., 139
Chen, C.-H., 221
Chesser, R. K., 437
Chovnick, A., 367
Chumley, F. G., 87
Cobbs, G., 381
Copeland, N. G., 169
Crow, J. F., 1
Cummings, M. P., 789
Curtis, D., 739

Dalton, M. W., 535
Damon, S., 181
Delosme, M., 335
Diehl, B. E., 287
Dimitri, P., 553
Drysdale, R., 497
Duttaroy, A., 367

Eppler, K., 637
Esch, J. J., 221

Fane, B., 263
Farrall, L., 87
Feilotter, H. P., 309
Ferrand, N., 799
Figueroa, F., 161
Foss, E. J., 711
Fox, T. D., 319
Fristrom, J. W., 747

Ganetzky, B., 497
Garrett, P. W., 711
Gaucci, V., 475
Gladstone, J., 583
Gonneau, M., 199
Gordon, L., 381
Gotwals, P. J., 747
Gray, M., 139

Haffter, P., 319
Harris, L. J., 205
Harris, S. D., 279
Hazelrigg, T., 125
Hellack, J. J., 117
Hewitt, J. D., 181
Higgins, D. R., 61
Hoff, G., 125
Horowitz, N. H., 631
Hudson, R. R., 565
Hughes, A. L., 345
Hughes, K. T., 657
Hutchinson, E. W., 719, 729
Hyde, D. R., 761

Jack, J., 151
Jenkins, N. A., 169
Jewell, L., 381
Jinks-Robertson, S., 53
Jones, C. W., 535
Jursnich, V. A., 525

Kaback, D. B., 475
Kallman, K. D., 399
Kamping, A., 507
Katzen, A. L., 367
Kaufman, T. C., 125
Keil, R. L., 31
King, J., 263
Kinsey, J. A., 711
Klar, A. J. S., 489
Klein, H. L., 75
Klein, J., 161
Konieczny, A., 801
Kreber, R., 497
Kreitman, M., 565
Kreuzer, K. N., 453
Kück, U., 335
Kurjan, J., 299

Lander, E. S., 181
Levin, D. M., 609
Lin, Y.-H., 31
Lincoln, S. E., 181
Link, A. J., 681
Liu, S., 151
Long, J. C., 417

Mackenzie, S. A., 411
Maruyama, T., 449
Masurekar, M., 453
McGill, C. B., 61
McLeod, E., 151
McMullin, T. W., 319
Menotti-Raymond, M., 355
Miller, J. H., 21
Moran, G. G., 619
Morizot, D. C., 399
Morris, M. E., 53
Mukai, T., 545
Muona, O., 619

Nasrallah, J. B., 221
Neff, M. W., 463
Nurse, P., 309

Olivera, B. M., 657
Olson, M. V., 681
Orzack, S. H., 583
O'Tousa, J. E., 761

Palladino, F., 75
Parker, E. D., Jr., 583
Parr, R., 637
Paterson, A. H., 181
Patterson, G. I., 205
Pelsy, F., 199
Petes, T. D., 39
Polyakov, A., 161
Pringle, J. R., 279, 287

Quattro, J. M., 391

Rabinowitch, H. D., 181
Rina, M., 769
Ripley, L. S., 453
Rogachova, M., 781
Rong, L., 75
Rose, M. R., 719, 729

Roth, J. R., 657
Ruvinsky, A., 161, 781

Sampson, L., 637
Sarkar, S., 257
Savakis, C., 769
Scandalios, J. G., 601
Schofield, M. A., 21
Selker, E. U., 699, 711
Shaw, A. J., 729
Silhavy, T. J., 671
Singer, M. J., 699
Siracusa, L. D., 169
Slatkin, M., 627
Slaugenhaupt, S. A., 399
Soriguer, R. C., 799
Spradling, A. C., 515
Stapleton, A., 39
Starmer, W. T., 355
Steele, D. F., 53
Strathern, J. N., 61
Suh, D.-S., 545
Sullivan, D. T., 355
Sweeney, R., 327
Szabad, J., 525

Tanksley, S. D., 181
Tantikanjana, T., 221
Thompson, J. N., Jr., 117
Thuerauf, D. J., 103
Tichy, H., 161
Townley, L. H., 535
Tucker, R. R., 117
Turelli, M., 229
Turlough, M. F., 5

Valent, B., 87
van Delden, W., 507
van der Loo, W., 789
VanWinkle-Swift, K. P., 103
Vihtelic, T. S., 761
Voelm, L., 627
Voytas, D. F., 789
Vrijenhoek, R. C., 391

Walbot, V., 205
Walsh, K., 139
Warmke, J., 497
Weinstock, K. G., 61
Weston-Hafer, K., 649
Whoriskey, S. K., 21
Williamson, J. D., 601
Wolfner, M. F., 125
Wu, C.-I., 429
Wu, P., 139
Wyckoff, E., 637

Yao, C.-H., 327
Yao, M.-C., 327
Young, P. G., 309

Zamir, D., 181

SUBJECT INDEX

to Volume 127, January–April 1991

Acacia melanoxylon, hierarchical patterns of correlated mating, 619
Acridine, -induced frameshift specificity in hotspot, topoisomerase-mediated DNA cleavage, bacteriophage T4, 453
Aging, postponed, *Drosophila melanogaster*, 719, 729
Alcohol dehydrogenase
  Adh and *adh-dup* loci, evolutionary histories, *Drosophila melanogaster*, 565
  Adh region of *Drosophila hydei*, structure and evolution, 355
Allele
  ectopic interactions and, recombination-defective yeast strains, 53
  SRS2/RADH gene, hyper-gene conversion *hpr5-1* mutation, yeast, 75
Aneuploidy, male-sex-ratio trait, *Drosophila pseudoobscura*, 381
Anniversay, diamond birthday of *Genetics*, 1
Arabidopsis thaliana, superfamily of retrotransposons, 801

Bacteriophage f1, gene *II* protein, novel recombinator, yeast, 61
Bacteriophage P22
  chromosome, map, gene *3* to *10* region, 637
  tailspike protein, intragenic suppressors, folding defects, 263
Bacteriophage T4, acridine-induced frameshift specificity in hotspot, toposiomerase-mediated DNA cleavage, 453
Behavior, social, gene diversity, female philopatry, 437
Brassica oleracea, second *S*-locus-related cDNA, 221
Bromodeoxyuridine, random segregation of chromatids, mitosis in yeast, 463

Catalase, *Cat2* and *Cat3*, photoregulation, maize leaves, 601
Cell cycle, analysis of *cdr1/nim1*, *Schizosaccharomyces pombe*, 309
Ceratitis capitata, cluster of vitellogenin genes, 769
Chlamydomonas monoica, mating-type evolution, sexual preferences, 103
Chlamydomonas reinhardtii, 335
Chromatids, random segregation, mitosis in yeast, 463
Chromosome
  authentic, distributive disjunction, yeast, 475
  bacteriophage P22, gene *3* to *10* region, 637
  lethal to gametophyte generation, maize, 609
  second
    changes in relative fitness with temperature, *Drosophila melanogaster*, 507
    heterochromatin, *Drosophila melanogaster*, 553
Chromosome *17*, mutations, tertiary trisomy, mouse, 781
Chromosome *I*
  mutagen specificity, temperature-sensitive-lethal mutations, yeast, 279
  transcribed regions that encode essential functions, yeast, 287
Chromosome *X*, balanced linkage of polygenes, natural population, *Drosophila*, 117
Circadian rhythm, *Cat2* and *Cat3* catalase, photoregulation, maize leaves, 601
Codon, cluster of vitellogenin genes, *Ceratitis capitata*, 769
Cold, sensitivity and anisomycin resistance, mutation in large unit ribosomal RNA gene, *Tetrahymena thermophila*, 327
Cytochrome *b*, resistance mutations, mitochondrial genetics, *Chlamydomonas reinhardtii*, 335
Cytoplasm, sterility-inducing, fertile accession line, *Phaseolus vulgaris*, 411

Deletion
  altered rates of formation, *Escherichia coli* mutants, 21
  illegitimate recombination, *Escherichia coli xonA*, 671
  nadC gene, *Salmonella typhimurium*, 657
  plasmid pBR322, replication slippage, leading and lagging strands, 649
Demes, F_{ST} in hierarchical island model, 627
DNA
  complementary, second *S*-locus-related, *Brassica oleracea*, 221
  denaturing gradient gel blots, point mutations, *Drosophila rosy* locus, 139
  genetic and physical map, gene *3* to *10* region, bacteriophage P22 chromsome, 637
  hotspot for meiotic recombination, Tn*3* β-lactamase gene, yeast, 39
  multiple origins of hybridogenic fish clones, *Poeciliopsis*, 391
  repeat-induced point mutation, *Neurospora crassa*, 699, 711
  repetitive probes for gene mapping, mouse, 169
  ribosomal, recombination in yeast mutations, RNA polymerase I-stimulated exchange, 31
  topoisomerase-mediated cleavage, acridine-induced frameshift specificity, bacteriophage T4, 453
Drosophila, 515, 535
Drosophila hydei, 355
Drosophila melanogaster, 117, 125, 139, 367, 497, 507, 525, 545, 553, 565, 719, 729, 739, 747, 761

Drosophila pseudoobscura, 381

Ecdysone, -inducible gene *E74*, structure and regulation, *Drosophila*, 535
Escherichia coli, 21, 671
Evolution
  Adh and *Adh-dup* loci, polymorphism, *Drosophila melanogaster*, 565
  Adh region of *Drosophila hydei*, 355
  conditional sex ratio behavior, genetic variation, *Nasonia vitripennis*, 583
  ecdysone-inducible gene *E74*, structure and regulation, *Drosophila*, 535
  gene diversity and female philopatry, 437

α-Factor, *MFα1* α-factor precursor and, mating in yeast, 299
Fertility, accession line of *Phaseolus vulgaris*, sterility-inducing cytoplasm, 411

Gametophyte, generation, segmental chromosomal transposition, maize, 609
Gene
  B-Peru regulatory, maize, 205
  Cat2 and *Cat3* catalase, photoregulation, maize leaves, 601
  cdr1/nim1, *Schizosaccharomyces pombe*, 309
  cell-proliferation control, *Drosophila* oogenesis, 525
  conversion, meiotic mutants *mei-9* and *mei-218*, 739
  E74, structure and regulation, *Drosophila*, 535
  eag, potassium channels, *Drosophila melanogaster*, 497
  flow, F_{ST} in hierarchical island model, 627
  II protein, novel recombinator in yeast, bacteriophage f1, 61
  mapping, repetitive probes, mouse, 169
  nadC, *Salmonella typhimurium*, 657
  pathogenicity and virulence, backcrosses, *Magnaporthe grisea*, 87
  retinal degeneration B, *Drosophila melanogaster*, 761
  SRS2/RADH, hyper-gene conversion *hpr5-1* mutation, yeast, 75
  Tn*3* β-lactamase, hotspot for meiotic recombination, yeast, 39
  3 to *10* region, map, bacteriophage P22 chromosome, 637
  vitellogenin, *Ceratitis capitata*, 769
Genome
  organelle, periodic selection, gene diversity, 449
  physical map, 110-kilobase resolution, yeast, 681

Heterochromatin, second chromosome, cytogenetic analysis, *Drosophila melanogaster*, 553
Homothallism, mating-type evolution, sexual preferences, *Chlamydomonas* mutant, 103
Hybrid dysgenesis, natural population, genetic variance of viability, *Drosophila melanogaster*, 545
Hyperplasia, cell-proliferation control genes, *Drosophila* oogenesis, 525

Imaginal disc, morphogenesis, *Broad-Complex* and *stubbloid* locus, *Drosophila melanogaster*, 747
Immunoglobulin, light chain, gene diversity at *b* locus, European rabbit, 789

Locus
  Broad-Complex and *stubbloid*, imaginal disc morphogenesis, *Drosophila melanogaster*, 747
  cut, cell type specification, *Drosophila*, 151
  doublesex, flanking regions, *Drosophila*, 125
  gene diversity at *b*, immunoglobulin light chain, European rabbit, 789
  natural and sexual selection, 229
  rosy, point mutations, *Drosophila melanogaster*, 139
  second *S*-locus-related cDNA, *Brassica oleracea*, 221
Luria-Delbrück distribution, Haldane's solution, 257

Magnaporthe grisea, genes for pathogenicity and virulence, series of backcrosses, 87
Maize
  chromosomes lethal to gametophyte generation, segmental chromosomal transposition, 609
  leaves, photoregulation, *Cat2* and *Cat3* catalase genes, 601
  regulatory gene, *B-Peru*, 205
Major histocompatibility complex, circumsporozoite protein genes, positive selection, *Plasmodium*, 345
Mapping
  genus *Xiphophorus*, 399
  quantitative traits, Mendelian factors, tomato, 181
  Saccharomyces cerevisiae genome, 110-kilobase resolution, 681
Maternal effect, cell-proliferation control genes, *Drosophila* oogenesis, 525
Mating
  correlated, hierarchical patterns, *Acacia melanoxylon*, 653
  mat1 interconversion, fission yeast, 489
  -type evolution, sexual preferences, *Chlamydomonas* mutant, 103
  yeast, α-factor and *MFα1* α-factor precursor, 299
Megaplasmid, 1600-kilobase *Rhizobium meliloti*, deletions generated *in vivo*, 5
Meiosis, distributive disjunction, authentic chromsomes, yeast, 475
Meiotic drive, autosomal aneuploid sperm, *Drosophila pseudoobscura*, 381
Mendelian factors, quantitative traits in tomato, 181
Mitochondria
  Chlamydomonas reinhardtii, resistance mutations, cytochrome *b* gene, 335
  ribosomal proteins, mRNA-specific translational activator, yeast, 319
  sterility-inducing cytoplasm, fertile accession line, *Phaseolus vulgaris*, 411

Mitosis
analysis of *cdr1/nim1*, *Schizosaccharomyces pombe*, 309
random segregation of chromatids, yeast, 463
Morphogenesis, regulatory regions of *cut* locus, cell type specification, *Drosophila*, 151
Mosaics, cell-proliferation control genes, *Drosophila* oogenesis, 525
Mouse
Eastern forms, low diversity, *t* haplotypes, 161
mutations of chromosome *17*, tertiary trisomy, 781
repetitive probes for gene mapping, 169
Mutagen, specificity, chromosome *I*, yeast, 279
Mutagenesis, topoisomerase-mediated DNA cleavage, acridine-induced frameshift specificity, bacteriophage T4, 453
Mutants
Drosophila melanogaster, *scalloped* region, 367
Escherichia coli, altered rates of deletion formation, 21
Escherichia coli xonA, illegitimate recombination, 671
folding defects, intragenic suppressors, P22 tailspike protein, 263
Haldane's solution, Luria-Delbrück distribution, 257
meiotic, gene conversion, *Drosophila melanogaster*, 739
molecular characterization of *eag*, *Drosophila melanogaster*, 497
Mutations
chromosome *I* in yeast, 279, 287
hpr5-1, hyper-gene conversion, allele of *SRS2/RADH* gene in yeast, 75
large subunit ribosomal RNA gene, anisomycin resistance and cold sensitivity, *Tetrahymena thermophila*, 327
Neurospora revolution of fifty years ago, 631
point, *rosy* locus, *Drosophila melanogaster*, 139
rDNA recombination in yeast, RNA polymerase I-stimulated exchange, 31
repeat-induced point, *Neurospora crassa*, 699, 711
resistance, cytochrome *b* gene, *Chlamydomonas reinhardtii*, 335

Nasonia vitripennis, genetic variation, conditional sex ratio behavior, 583
Neoplasia, cell-proliferation control genes, *Drosophila* oogenesis, 525
Neurospora crassa, 631, 699, 711
Nicotiana plumbaginifolia, nitrate reductase apoenzyme-deficient mutants, intragenic complementation events, 199

Oogenesis, *Drosophila melanogaster*, cell-proliferation control genes, 525
Organelle, genomes, periodic selection, gene diversity, 449
Oryctolagus cuniculus, Ig allotype diversity, 789

Pathogenicity, gene for virulence, backcrosses, *Magnaporthe grisea*, 87
P element
scalloped region, *Drosophila melanogaster*, 367
transposition, rate and site-specificity, *Drosophila*, 515
Phaseolus vulgaris, fertile accession line, sterility-inducing cytoplasm, 411
Pheromone, α-factor and *MFα1* α-factor precursor, mating in yeast, 299
Philopatry, female, gene diversity, 437
Photoreceptor, *retinal degeneration B* gene, *Drosophila melanogaster*, 761
Phylogeny, species, relation to segregation, ancient polymorphisms, 429
Plasmid, pBR322, replication slippage, leading and lagging strands, 649
Plasmodium, circumsporozoite protein genes, positive selection, immunogenic regions, 345
Poeciliopsis, multiple origins of hybridogenetic fish clones, 391
Pollen, hierarchical patterns of correlated mating, *Acacia melanoxylon*, 619
Polygenes, balanced linkage of *X* chromosome, natural population, *Drosophila*, 117
Polymorphism
ancient, species phylogeny in relation to segregation, 429
changes in relative fitness with temperature, second chromosome arrangements, *Drosophila melanogaster*, 507
evolutionary histories of *Adh* and *Adh-dup* loci, *Drosophila melanogaster*, 565
Population
admixed, genetic structure, 417
F_{ST} in hierarchical island model, 627
natural
balanced linkage of *X* chromosome, *Drosophila*, 117
hybrid dysgenesis, *Drosophila melanogaster*, 545
Ig allotype diversity, European rabbit, 789
Potassium channels, molecular characterization of *eag*, *Drosophila melanogaster*, 497
Protein kinase, analysis of *cdr1/nim1*, *Schizosaccharomyces pombe*, 309

Quinolinic acid, *nadC* gene, *Salmonella typhimurium*, 657

Recombination
-defective yeast strains, allelic and ectopic interactions, 53
gene conversion, meiotic mutants, *Drosophila melanogaster*, 739
illegitimate, *Escherichia coli xonA*, 671
1600-kilobase *Rhizobium meliloti* megaplasmid, dele-

tions generated *in vivo*, 5
meiotic, Tn*3* β-lactamase gene, yeast, 39
rDNA, RNA polymerase I-stimulated exchange, mutations in yeast, 31
repeat-induced point mutation, *Neurospora crassa*, 699, 711
without, periodic selection, gene diversity in organelle genomes, 449
Replication
fission yeast mating type interconversion, 489
slippage, deletions, plasmid pBR322, 649
Retina, *retinal degeneration B* gene, *Drosophila melanogaster*, 761
Retrotransposons, superfamily of *Arabidopsis thaliana*, 789
Rhizobium meliloti, 1600-kilobase megaplasmid, deletions generated *in vivo*, 5
Ribosomal proteins, mitochondrial, mRNA-specific translational activator, yeast, 319
RNA, large subunit ribosomal gene, anisomycin resistance and cold sensitivity, *Tetrahymena thermophila*, 327
RNA polymerase I, -stimulated exchange, rDNA recombination in yeast, mutations, 31

Saccharomyces cerevisiae, 31, 39, 53, 75, 279, 287, 299, 319, 463, 475, 489, 681
Salmonella typhimurium, *nadC* gene, 657
Schizosaccharomyces pombe, analysis of *cdr1/nim1*, 309
Selection
changes in relative fitness with temperature, second chromosome arrangements, *Drosophila melanogaster*, 507
conditional sex ratio behavior, genetic variation, *Nasonia vitripennis*, 583
evolutionary histories of *Adh* and *Adh-dup*, polymorphism, *Drosophila melanogaster*, 565
natural and sexual, many loci, 229
periodic, gene diversity, organelle genomes, 449
positive, circumsporozoite protein genes, *Plasmodium*, 345
Sex ratio
autosomal aneuploid sperm, *Drosophila pseudoobscura*, 381
conditional behavior, genetic variation, *Nasonia vitripennis*, 583
Sexual differentiation, *doublesex* locus of *Drosophila melanogaster*, flanking regions, 125
Sperm, autosomal aneuploid, male-sex-ratio trait, *Drosophila pseudoobscura*, 381
Sterility, -inducing cytoplasm, fertile accession line, *Phaseolus vulgaris*, 411
Suppressors, intragenic, folding defects, P22 tailspike protein, 263
Temperature, changes in relative fitness, *Drosophila melanogaster*, 507
Tetrahymena thermophila, mutations in large subunit ribosomal RNA gene, anisomycin resistance, cold sensitivity, 327
t haplotypes, low diversity, Eastern form, house mouse, 161
Tomato, quantitative traits, Mendelian factors, 181
Topoisomerase, -mediated DNA cleavage, acridine-induced frameshift specificity, bacteriophage T4, 453
Translation, mRNA-specific translational activator, mitochondrial ribosomal proteins, yeast, 319
Transposition
P element, rate and site-specificity, *Drosophila*, 515
segmental chromosome, gametophyte generation, maize, 609
Transposons, 1600-kilobase *Rhizobium meliloti* megaplasmid, deletions generated *in vivo*, 5
Trisomy, tertiary, mutations of chromosome *17*, mouse, 781

Virulence, gene for, backcrosses, *Magnaporthe grisea*, 87
Vision, *retinal degeneration B* gene, *Drosophila melanogaster*, 761
Vitellogenin, gene cluster, *Ceratitis capitata*, 769

Xiphophorus, genetic linkage maps of fishes, 399

Yeast
chromosome *I*
mutagen specificity, temperature-sensitive-lethal mutations, 279
transcribed regions, essential functions, 287
distributive disjunction of authentic chromosomes, 475
fission, mating type interconversion, 489
hyper-gene conversion *hpr5-1* mutation, allele of *SRS2/RADH* gene, 75
mating, α-factor and *MFα1* α-factor precursor, 299
mitochondrial ribosomal proteins, functional interactions, mRNA-specific translational activator, 319
mitosis, random segregation of chromatids, 463
novel recombinator, gene *II* protein, bacteriophage f1, 61
physical map of genome, 110-kilobase resolution, 681
rDNA recombination, mutations, RNA polymerase I-stimulated exchange, 31
recombination-defective strains, allelic and ectopic interactions, 53